

FIG. 1.

[illegible]

MATCH WITH FIG. 1B

096522

11-6-11

-----+ 360

GGTTGGAGCTTGAGTTCCCTGTCTTCTCTGATATTTTAAACGACGTCGTGTAATATTATGTC  
N L N S R T E E T I K F A A A H Y N T E -

AGATCTTGAAGAATTGATAATGAGTGAGAAAGACTCAATGCCACGGGAGGT  
-----+-----+-----+-----+-----+-----+ 420

TCTAGACTTTTCATTACTATTACTCACCCTCTTTCTGAGTTACGTACGGTGCCCTCCACA  
 I L K S I D N E W R K T Q C M P R E V C -

GTATAGATGTTGGGAAGGAGTTGGAGTCGCCACAACACTTCTTTAAACCTCCATGTC  
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480

CATATCTACACCCCTTCTCTCAAACCTCAGCGCTGTTGTGGAAGAATTGGAAGTACAC  
 I D V G K E ' F G V A T N T F F K P P C V -

[illegible]

ACAGGCAGATGTTACACCCCCAACGAGTTATCACTCCCGAGCTCACGTA

GCACGAGCTACCTCAGCAGACGTTATTGAAATTACAGTGCCTCTCTCAAGCCCCA 600

CGTGCCTCGATGGAGTCGTTCTGCAATAACTTTAATGTCACGGAGAGAGAGTTCGGGGT  
T S Y L S K T L F E I T V P L S O G P K -

AACCGTAACAATCAGTTTCCCAATCACACTTCTCCGATGCATGCTAAACTGATG 650

TTGGTCATTGTTAGTCAAAACGGTTAGTGTGAAGACGGCTACGTACAGATTGACCTAC  
P V T I S F A N H T S C B C M S K L D V -

# MATCH WITH FIG 1c

MATCH WITH FIG. 1B

FIG. 1C

661

TTTACAGACAAGTTCATTCCATTATAGACGTTCCCTGCCAGCAACACTACCACAGTGTCTC

720

AAATGCTCTGTCAAGTAAGGTAATTAATCTGCAAGGACGGTGTGTGATGCTGCACAG

C Y R Q V H S I I R S L P A T L P Q C Q -

721

AGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATTAATCACAATCTGCAGATGCC

780

TCCGTCGCTTGTCTTGACCGGGGTGTTAATGTACACCTTAATTAAGTGTAGACGCTTACCG

C A A N K T C P T N Y M W N N H I C R C L -

781

TGGCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGAGATGACTCAACAGATGATTC

840

ACCGAGTCCTTCTAATAAATACAAAGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG

C A Q E D F M F S S D A G D D S T D G F H -

841

ATGACATCTGTGACCAACAAGAGAGCTGATGAAGAGACCTGTCACTGTGTCTGCAGAG

900

TACTGTAGACACCTGTTGTTTCTCCTCGACCTACTTCTCTGACAGTCAACAGACGTCTC

C D I C G P N K E L D E E T C Q C V C R A -

901

CGGGCTTCGGCCTGCCAGCTGTGGAACCCACAAGAAGACTAGACAGAACTCATGCCAGT

960

GCCCCGAAGCCGGAACGGTGCACACCTGGGGTGTCTTGAATCTGTCTTGAAGTACGGTCA

C G L R P A S C G P H K E L D R N S C Q C -

961

GTGTCTGTAATAACAACCTCTTCCCAAGCCAATGTGGGCCAACCGAGAATTGTATGAAA

1020

CACAGACATTTTGTGTGAGAAGGGGTGCTTACACCCCGTTGGCTCTTAACACTACTTT

MATCH WITH FIG. 1D

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# MATCH WITH FIG. 1C FIG. 1D

C V C K N K L F P S Q C G A N R E F D E N -

1021 ACACATGCCAGTGTGTATGTAAGAACCCTGCCCAAGAATCAACCCCTAATCCTGAA + 1080

C TGTGTACGGTCACACATACATTTTCTTGGACGGGCTTTAGTTGGGATTTAGACCTT  
T C Q C V C K R T C P R N Q P L N P G K -

1081 AATGTCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAGAAGAAGTTC + 1140

C TTACACGGACACTTACATGTCTTTACAGGTGTCTTTACGAACAATTTCTTCTCAAG  
C A C E C T E S P Q K C L L K G K K F H -

1141 ACCACCAACATGCAGCTGTACAGACGGCCATGTACGAACCGCCAGAAGCTTGTGAC + 1200

C TGGTGGTTTGTACGTGACAATGTCTGCCGTACATGCTTGGCGTCTTCGAACACTCG  
H Q T C S C Y R R P C T N R Q K A C E P -

1201 CAGGATTTTCATATAGTGAAGAAGTGTGTGTCCTTCATATTTGCCAAAGACCAC + 1260

C GTCCTAAGAAGTATATCCTTCTTACACACGAACAGGAAGTATAACCGTTTCTGCTG  
G F S Y S E E V C R C V P S Y W Q R P Q -

AAATGAGCTAAGATTGTACTGTCTTCCAGTTCATCGATTCTTCTATTATGAAAACTGTGT

MATCH WITH FIG. 1E

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Fig. 1

○

1 CGAGCCACGGCTTATGCAAGCAAGATCTGGAGGACGATTACGGTCTGTGCCAGTGT  
-----+-----+-----+-----+-----+-----+-----+  
71 AGATGAACTCATGACTGTACTCTACCCAGAATATTGAAAATGTACAAGTGTCAAGCTAAG  
-----+-----+-----+-----+-----+-----+-----+  
M T V L Y P E Y W K M Y K C Q L R  
-----+-----+-----+-----+-----+-----+-----+  
121 GAAAGAGGCTGGCAACATTAACAGAGAACAGGCCAACCCTCAACTCAAGGACAGAGAGAC  
-----+-----+-----+-----+-----+-----+-----+  
K G G W Q H N R E Q A N L N S R T E E T  
-----+-----+-----+-----+-----+-----+-----+  
181 TATAAAATTGTCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTC  
-----+-----+-----+-----+-----+-----+-----+  
I K F A A A H Y N T E I L K S I D N E W  
-----+-----+-----+-----+-----+-----+-----+  
241 GAGAAAGACTCAATGCATGCCACGGGAGGTGTATAGATGTGGGAAGGAGTTTGAGT  
-----+-----+-----+-----+-----+-----+-----+  
R K T Q C M P R E V C I D V G K E F G V  
-----+-----+-----+-----+-----+-----+-----+  
301 CGCGACAACACCTTCTTTAAACCTCCATGTGTGTCCGCTACAGATGTGGGGTTGCTC  
-----+-----+-----+-----+-----+-----+-----+  
A T N T F F K P P C V S V Y R C G C C C

FIG. 2A

361 CAATAGTGAGGGCTGCAGTGCATGAACACGACGAGCTACTCAGCAAGCGTTATT  
 -----+-----  
 N S E G L Q C M N T S T S Y L S K T L F  
 421 TGAATTTACAGTGCCCTCTCTCAAGCCCCAACCAGTAACAATCAGTTTGGCAATCA  
 -----+-----  
 E I T V P L S Q G P K P V T I S F A N H  
 481 CACTTCCCTGCCGATGCATGTCTAAACTGCGATTTTACAGACAAGTTTCATTATTTAG  
 -----+-----  
 T S C R C M S K L D V Y R Q V H S I I R  
 541 ACCTTCCCTGCCAGCAACACTACCACAGTGTCAAGCAGCGAACAAGACCTGCCCAACCA  
 -----+-----  
 R S L P A T L P Q C Q A A N K T C P T N  
 601 TTACATGTGAATAATCACAATCTGCAGATGCCCTGGCTCAGGAAGATTTATGTTTCTC  
 -----+-----  
 Y M W N N H I C R C L A Q E D F M F S S  
 661 GGATGCTGGAGATGACTCAACAGATGATTCATGACATCTGTGACCAACAAGAGCT  
 -----+-----  
 D A G D D S T D G F H D I C G P N K E L

FIG.2B

721 GGATGAGAGACCTGTCAGTGTCTGTCAGAGCGGGCTTCCGCCCTGCCAGCTGTGACC  
 -----+-----  
 D E E T C Q C V C R A G L R P A S C G P  
 -----+-----  
 781 CCACAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTAAACAACTCTTCCCAG  
 -----+-----  
 H K E L D R N S C Q C V C K N K L F P S  
 -----+-----  
 841 CCAATGTGGGGCCACCGAGAAATTGATGAACACATGCCAGTGTGTATGTAAAGAAC  
 -----+-----  
 Q C G A N R E F D E N T C Q C V C K R T  
 -----+-----  
 901 CTGCCCCAGAAATCAACCCCTTAATCCTGGAAATGTCCTGTGAATGTACAGAAAGTCC  
 -----+-----  
 C P R N Q P L N P G K C A C E C T E S P  
 -----+-----  
 961 ACAGAAATGCTTGTAAAGGAAGAAGTTCCACCACCAACATGCAGCTGTACAGACG  
 -----+-----  
 Q K C L L K G K K F H H Q T C S C Y R R  
 -----+-----  
 1021 GCCATGTACGAACCGCCAGAAAGCCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG  
 -----+-----  
 P C T N R Q K A C E P G F S S E E V C  
 -----+-----

FIG. 2C



1081 TCGTTGTGTCCTTCATATTGGCAAGACCACAATGAGCTAAGATTGTTACTGTTTCCA  
-----+-----+-----+-----+-----+  
R C V P S Y W Q R P Q M S  
-----+-----+-----+-----+-----+  
1141 GTTCATCGATTCTTCTATTATGAAACTGTGTGCGCACAGTAGAACTGTCTGTGAACAGA  
-----+-----+-----+-----+-----+  
1201 GAGACCCCTTGTGGGTCATGCTAACAAAGACAAGTCTGTCTTCCCTGAACCATGTGA  
-----+-----+-----+-----+-----+  
1261 TAACTTTACAGAAATGGA CTGGAGCTCATCTGCAAAAGCCCTCTTGTAAGACTGTTTT  
-----+-----+-----+-----+-----+  
1321 CTGCCAATGACCACAACGCCAAGATTTCCTCTGTGATTTCCTTAAAGAATGACTATA  
-----+-----+-----+-----+-----+  
1381 TAAATTTATTTCCACTAAAAATATTGTTCTGCAATTTTATAGCAACAATTCGT  
-----+-----+-----+-----+-----+  
1441 AAAACTCACTGTGATCAATATTTTATATCATGCCAAAATATGTTTAAATAAATGAAAA  
-----+-----+-----+-----+-----+  
1501 TTGTATTATAAAAAAAAAAAAAAA  
-----+-----+-----+-----+-----+

FIG. 2D

1  
50

Pdgfa .MRTIACLL LGGYLAHVL AEEAIPREV IERLARSQIH SIRDLOLLE  
 Pdglb MNRCWA.LEL SLCCYLRLVS AEGDPIPEEL YEMLSDEHIS SFDDLQRLLE  
 Vegf .....MNFLL SWVHWSIALLL LY.....  
 Vegf2 .....MTV LYPEYWKMYK CQ..... .LRKGWQH

51 100

Pdgfa IDSVGSEDSL DTSLRAHGVH ATKHVPEKRP LPIRRKRSI. ....EEAVP  
 Pdglb GDP.GEEDGA ELDLNMTRSH SGGELES... .LARGRSLG SLTLAEPAMI  
 Vegf APMAE..... .GGGQ NHHEVVKFMD .VYQR.....  
 Vegf2 REQANLNSRT EETIKFAAAH YNTEILKSID NEWRK.....

101 150

Pdgfa AVCKTRTVIY EIPRSQVDPT SANFLIMPPC VEVKRCCTGCC NTSSVKCPDS  
 Pdglb AECCKTRTEVF EISRLIDRT NANFLVWPBC VEVQRCSGCC NNRNVQCRPT  
 Vegf SYCHPIETLV DIFQEYRDEI ..EYIFKPSV PLMRCGGCC NDEGLECVPT  
 Vegf2 TQCMPREVCI DVGKEFGVAT ..NTFFKPPC VSVYRCGGCC NSEGLQCMNT

151 200

Pdgfa RVHHRSVKVA KVEYVRKKPK LKEVQVRLEE HLECCAC..... AT.....  
 Pdglb QVQLRPVQVR KIEIVRKKPI FKKAIVTLED HLAACK..... ETVAARPVV  
 Vegf EESNITMQIM RIK.PH..QG QHIGEMSFLO HNKCECRPKK DRARQEKKS  
 Vegf2 STSYLSKTLF EIT.VPLSQG PKPVTISPAN HTSCRCMSKL DVYRQVHSII

FIG. 3A

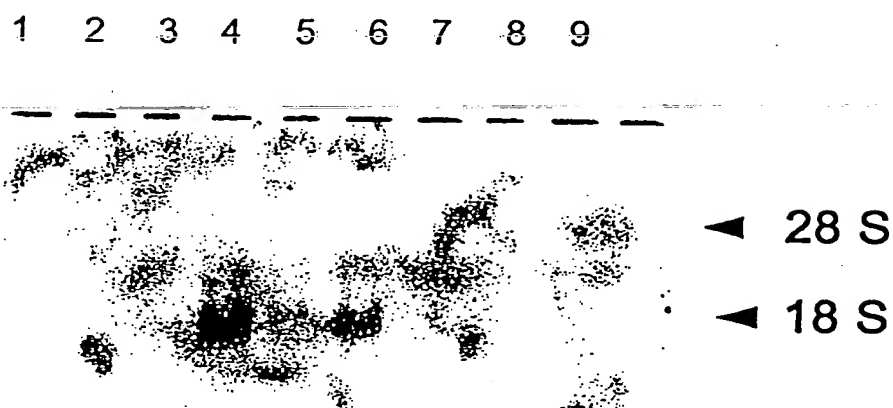
	201		250
Pdgfa	....TSLNPD YREEDTDVR.	.....	.....
Pdgfb	RSPGGSQEQR AKTPQTRVTI RTVRVRBPX GKHKPKHTH DKTALKETLG		
Vegf	RGR.....	.GKGQKKRKX KSRYSWSVY VGARCCIMPW SLPGPH...	
Vegf2	RRSLPATLPQ CQANKTCPT NYMNNHICR CLAQEDFMFS SDAGDDSTDG		
	251		300
Pdgfa	.....	.....	.....
Pdgfb	A.....	.....	.....
Vegf	....CGP...	.....	.....
Vegf2	FHDICGPNKE LDEETCQCVC RAGLRPASCX PHKEL...DR NSCQCVCXNK		
	301		350
Pdgfa	.....	.....	.....
Pdgfb	.....	.....	.....
Vegf	..DSRCARQ LEINERTCRC DKPRR.....		
Vegf2	LFPSQCGANR .EPDENTCQC VCKRTCPRNQ PLNPGKACX CTESPOKCLL		
	351		398
Pdgfa	.....	.....	.....
Pdgfb	.....	.....	.....
Vegf	.....	.....	.....
Vegf2	KGKKFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRGVPS YWQRPQMS		

FIG. 3B

PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN EACH PAIR OF GENES IS SHOWN IN THE FOLLOWING TABLE				
	PDGF $\alpha$	PDGF $\beta$	VEGF	VEGF2
PDGF $\alpha$				
PDGF $\beta$	48.0			
VEGF	20.7	22.7		
VEGF2	23.5	22.4	30.0	

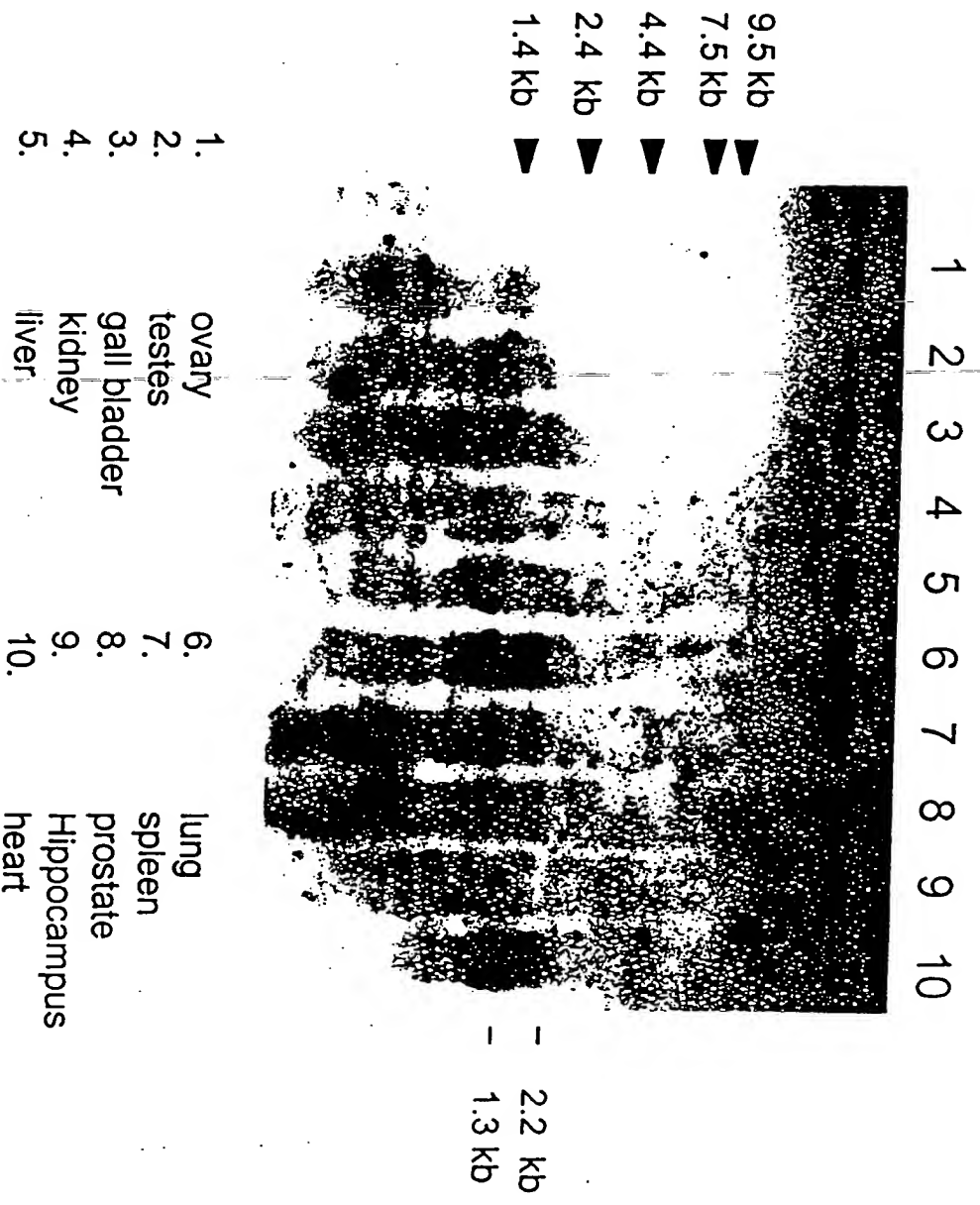
FIG. 4

Expression of VEGF2 mRNA in  
Human Breast Tumor Cells



1. normal breast tissue
2. breast tumor tissue
- 3-9. breast tumor cell lines.

FIG. 5

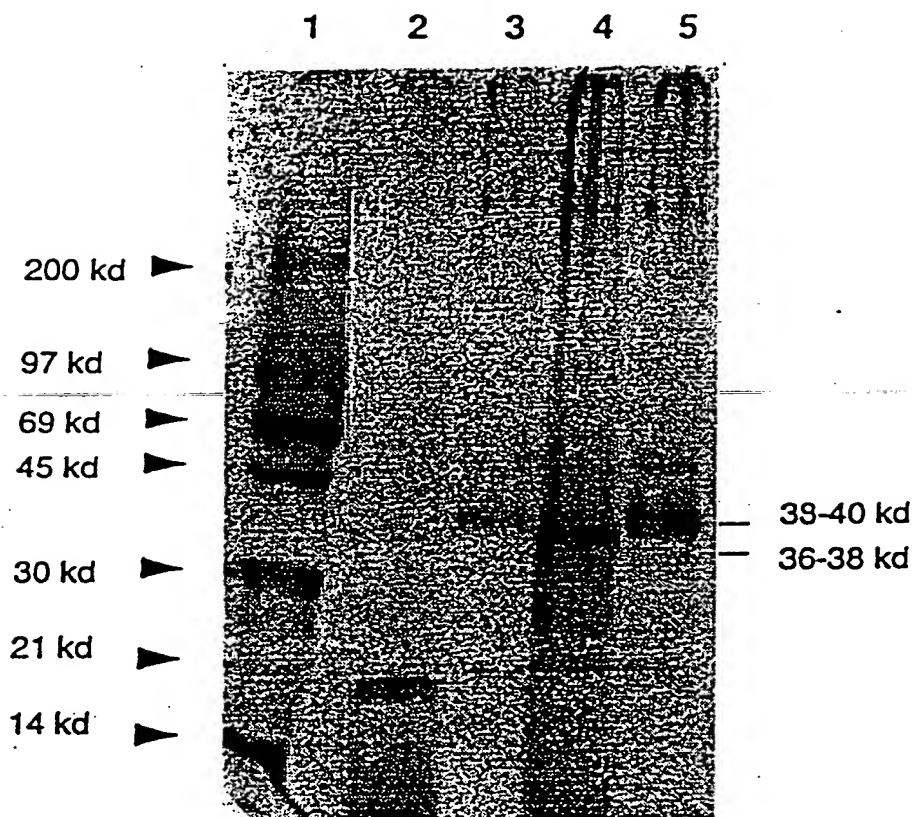


Expression of VEGF2 mRNA in human adult tissues.

FIG. 6

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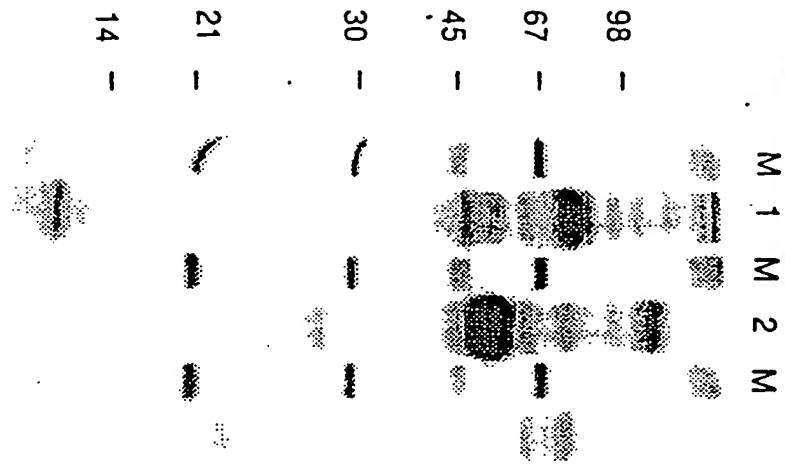
# FIG. 7



- Lane 1: 14-C and rainbow M.W. marker
- Lane 2: FGF control
- Lane 3: VEGF2 (M13-reverse & forward primers)
- Lane 4: VEGF2 (M13-reverse & VEGF-F4 primers)
- Lane 5: VEGF2 (M13-reverse & VEGF-F5 primers)

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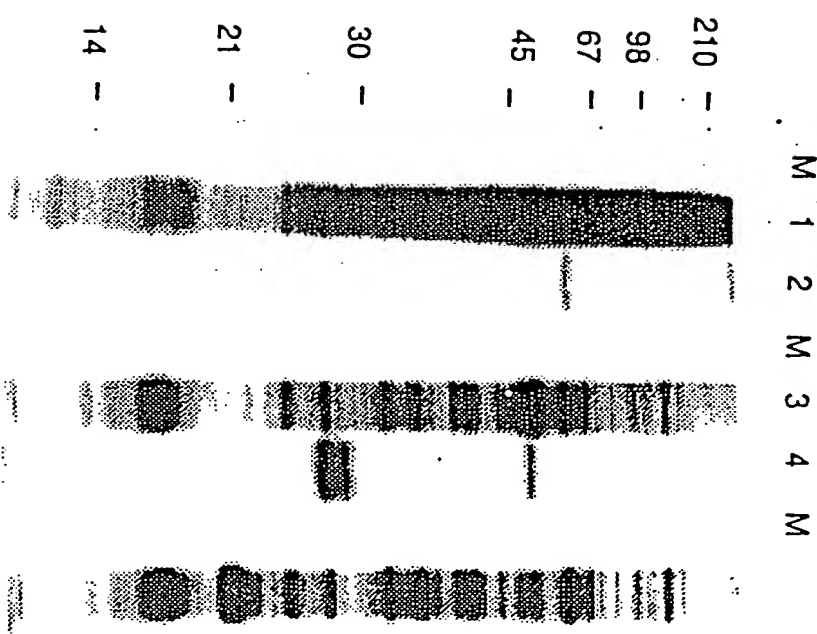
non-reducing gel



Lane M: Marker  
 Lane 1: vector medium  
 Lane 2: VEGF2 medium

FIG. 8A

reducing gel



Lane M: Marker  
 Lane 1: vector cytoplasm  
 Lane 2: vector medium  
 Lane 3: VEGF2 cytoplasm  
 Lane 4: VEGF2 medium

FIG. 8B



FIG. 9

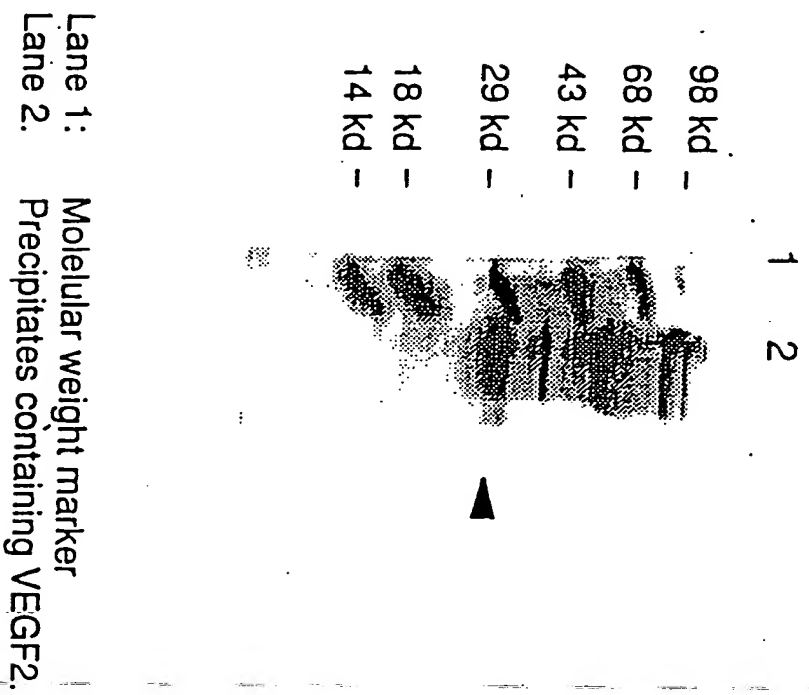
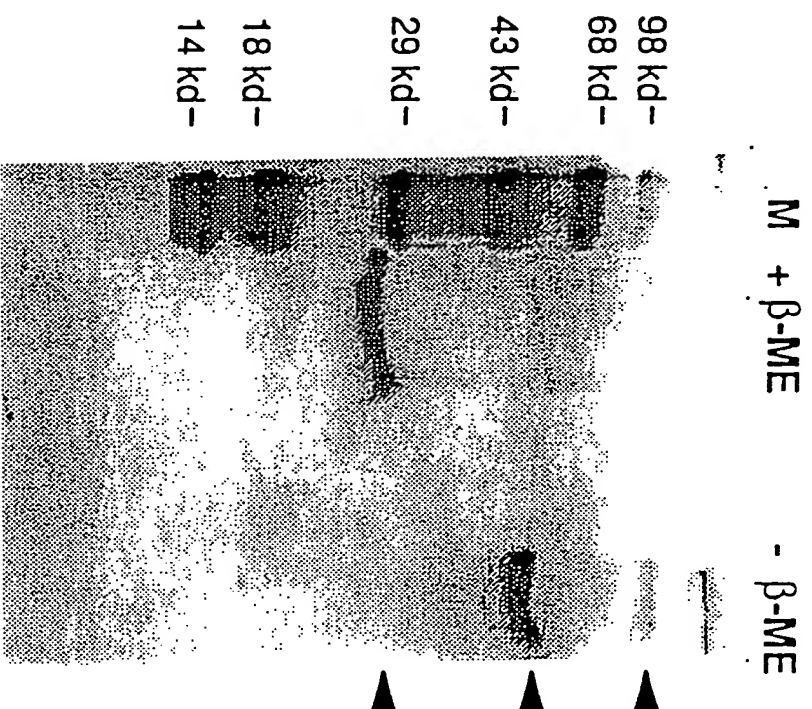
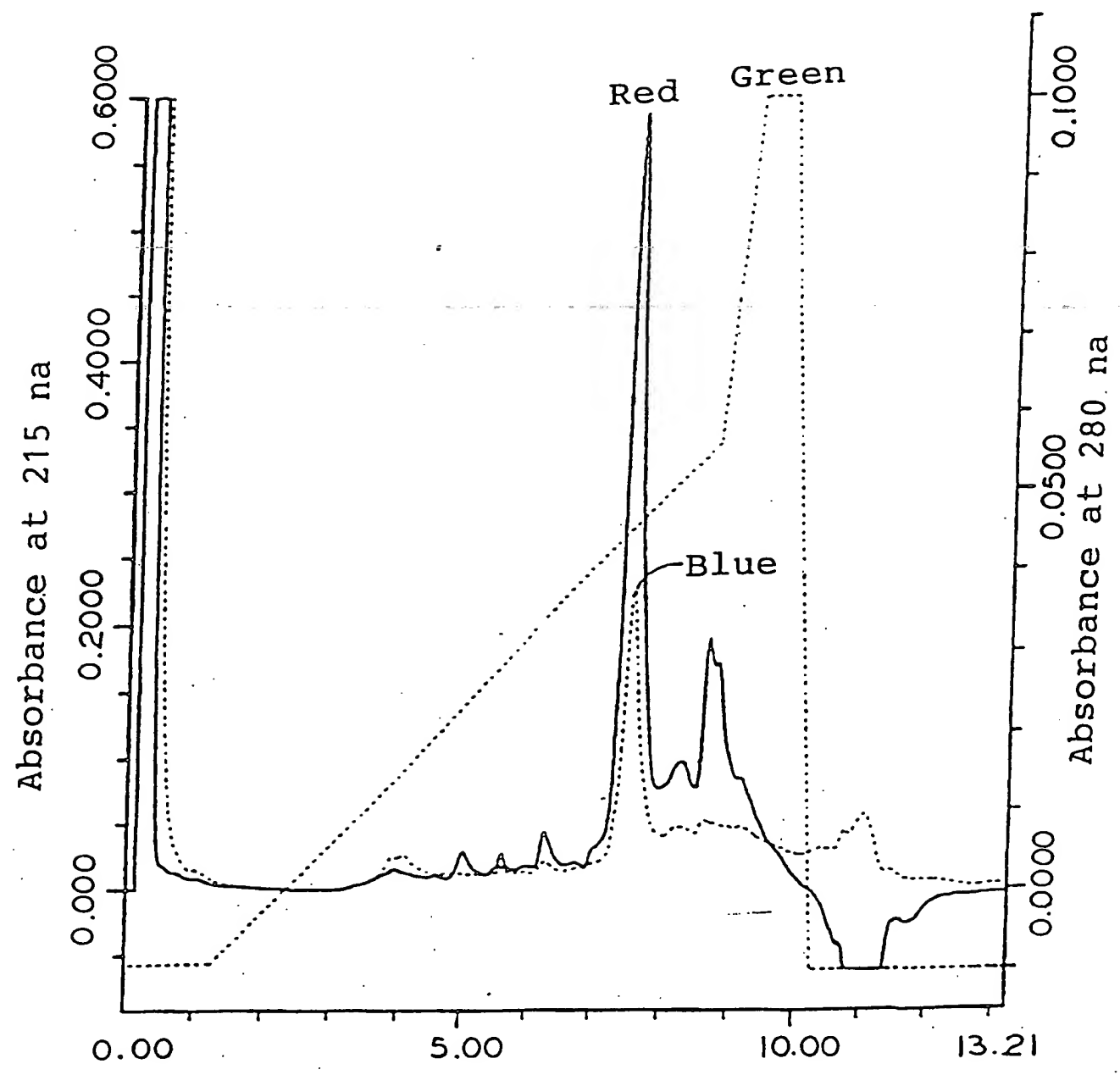


FIG. 10



665220" 2225260

FIG. 11



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FIG. 12

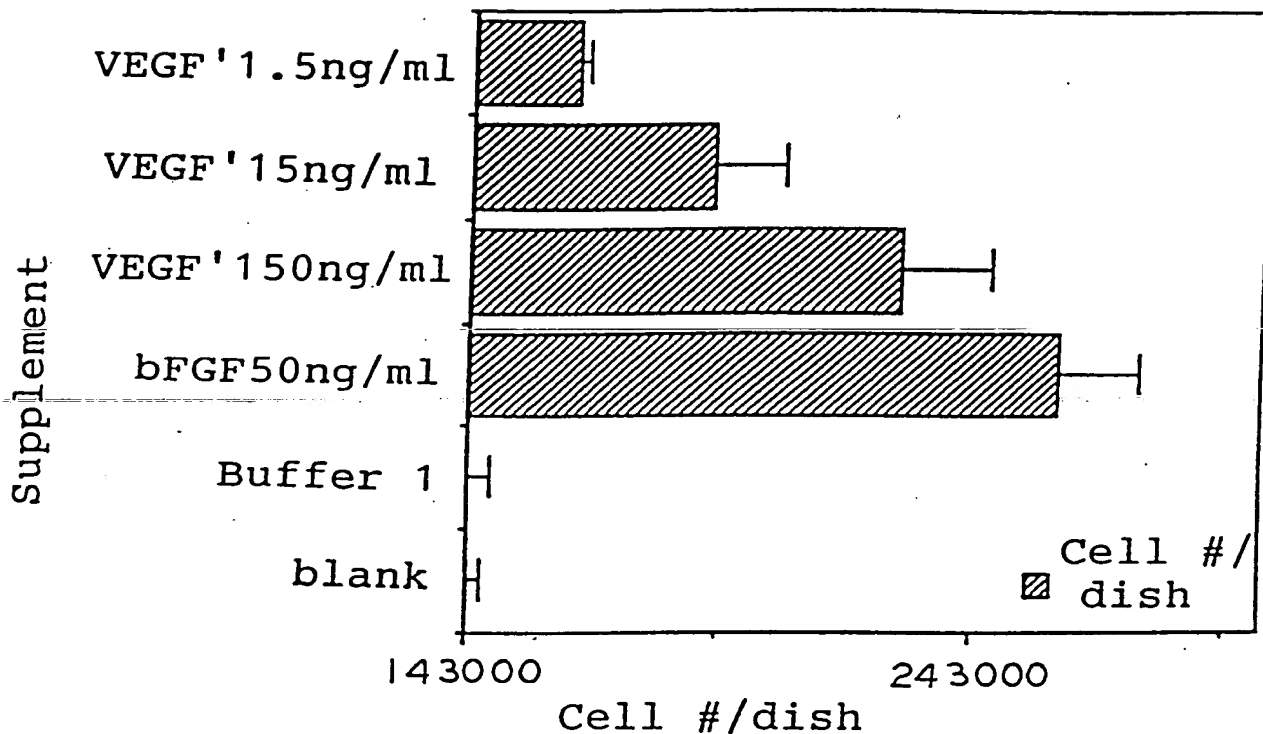


FIG. 13

